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1
SEQUENCE LISTING

<110> Sema ApS

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Christensen, Claus

Lukanidin, Eugene

Olesen, Ole

<120> Use of compounds capable of inhibiting the proteolytic processing of semaphorins for prevention, treatment, diagnosis and prognosis of an invasive disease

<130> P682 PC00

<160> 30

<170> PatentIn version 3.1

<210> 1

<211> 775

<212> PRT

<213> mouse Sema3E Genbank#Z93948

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Asp Asn Lys Met Tyr Phe Phe Phe Thr Glu Lys Ala Leu Glu Ala Glu
 245 250 255

Asn Asn Ala His Thr Ile Tyr Thr Arg Val Gly Arg Leu Cys Val Asn
 260 265 270

Asp Met Gly Gly Gln Arg Ile Leu Val Asn Lys Trp Ser Thr Phe Leu
 275 280 285

Lys Ala Arg Leu Val Cys Ser Val Pro Gly Met Asn Gly Ile Asp Thr
 290 295 300

Tyr Phe Asp Glu Leu Glu Asp Val Phe Leu Leu Pro Thr Arg Asp Pro
 305 310 315 320

Lys Asn Pro Val Ile Phe Gly Leu Phe Asn Thr Thr Ser Asn Ile Phe
 325 330 335

Arg Gly His Ala Val Cys Val Tyr His Met Ser Ser Ile Arg Glu Ala
 340 345 350

Phe Asn Gly Pro Tyr Ala His Lys Glu Gly Pro Glu Tyr His Trp Ser
 355 360 365

Leu Tyr Glu Gly Lys Val Pro Tyr Pro Arg Pro Gly Ser Cys Ala Ser
 370 375 380

Lys Val Asn Gly Gly Lys Tyr Gly Thr Thr Lys Asp Tyr Pro Asp Asp
 385 390 395 400

Ala Ile Arg Phe Ala Arg Ile Asp Pro Leu Met Tyr Gln Pro Ile Lys
 405 410 415

Pro Val His Lys Lys Pro Ile Leu Val Lys Thr Asp Gly Lys Tyr Asn
 420 425 430

Leu Arg Gln Leu Ala Val Asp Arg Val Glu Ala Glu Asp Gly Gln Tyr
 435 440 445

Asp Val Leu Phe Ile Gly Thr Asp Thr Gly Ile Val Leu Lys Val Ile

450 455 460
 Thr Ile Tyr Asn Gln Glu Thr Glu Trp Met Glu Glu Val Ile Leu Glu
 465 470 475 480
 Glu Leu Gln Ile Phe Lys Asp Pro Ala Pro Ile Ile Ser Met Glu Ile
 485 490 495
 Ser Ser Lys Arg Gln Gln Leu Tyr Ile Gly Ser Ala Ser Ala Val Ala
 500 505 510
 Gln Val Arg Phe His His Cys Asp Met Tyr Gly Ser Ala Cys Ala Asp
 515 520 525
 Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ile Ser Cys
 530 535 540
 Ser Arg Tyr Tyr Pro Thr Gly Ala His Ala Lys Arg Arg Phe Arg Arg
 545 550 555 560
 Gln Asp Val Arg His Gly Asn Ala Ala Gln Gln Cys Phe Gly Gln Gln
 565 570 575
 Phe Val Gly Asp Ala Leu Asp Arg Thr Glu Glu Arg Leu Ala Tyr Gly
 580 585 590
 Ile Glu Ser Asn Ser Thr Leu Leu Glu Cys Thr Pro Arg Ser Leu Gln
 595 600 605
 Ala Lys Val Ile Trp Phe Tyr Gln Lys Gly Arg Asp Val Arg Lys Glu
 610 615 620
 Glu Val Lys Thr Asp Asp Arg Val Val Lys Met Asp Leu Gly Leu Leu
 625 630 635 640
 Phe Leu Arg Val Arg Lys Ser Asp Ala Gly Thr Tyr Phe Cys Gln Thr
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 Val Glu His Asn Phe Val His Thr Val Arg Lys Ile Thr Leu Glu Val
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Glu Arg His His Lys Met Pro Cys Pro Pro Leu Ser Gly Met Ser Gln
690 695 700

Gly Thr Lys Pro Trp Tyr Lys Glu Phe Leu Gln Leu Ile Gly Tyr Ser
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Asn Phe Gln Arg Val Glu Glu Tyr Cys Glu Lys Val Trp Cys Thr Asp
725 730 735

Lys Lys Arg Lys Lys Leu Lys Met Ser Pro Ser Lys Trp Lys Tyr Ala
740 745 750

Asn Pro Gln Glu Lys Arg Leu Arg Ser Lys Ala Glu His Phe Arg Leu
755 760 765

Pro Arg His Thr Leu Leu Ser
770. 775

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<211> 775

<212> PRT

<213> human SEMA3E Genbank#NM012431

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20 25 30

Leu Arg Leu Ser His Lys Glu Leu Leu Asn Leu Asn Arg Thr Ser Ile
35 40 45

Phe His Ser Pro Phe Gly Phe Leu Asp Leu His Thr Met Leu Leu Asp
 50 55 60

Glu Tyr Gln Glu Arg Leu Phe Val Gly Gly Arg Asp Leu Val Tyr Ser
 65 70 75 80

Leu Ser Leu Glu Arg Ile Ser Asp Gly Tyr Lys Glu Ile His Trp Pro
 85 90 95

Ser Thr Ala Leu Lys Met Glu Glu Cys Ile Met Lys Gly Lys Asp Ala
 100 105 110

Gly Glu Cys Ala Asn Tyr Val Arg Val Leu His His Tyr Asn Arg Thr
 115 120 125

His Leu Leu Thr Cys Gly Thr Gly Ala Phe Asp Pro Val Cys Ala Phe
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Ile Arg Val Gly Tyr His Leu Glu Asp Pro Leu Phe His Leu Glu Ser
 145 150 155 160

Pro Arg Ser Glu Arg Gly Arg Gly Arg Cys Pro Phe Asp Pro Ser Ser
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Ser Phe Ile Ser Thr Leu Ile Gly Ser Glu Leu Phe Ala Gly Leu Tyr
 180 185 190

Ser Asp Tyr Trp Ser Arg Asp Ala Ala Ile Phe Arg Ser Met Gly Arg
 195 200 205

Leu Ala His Ile Arg Thr Glu His Asp Asp Glu Arg Leu Leu Lys Glu
 210 215 220

Pro Lys Phe Val Gly Ser Tyr Met Ile Pro Asp Asn Glu Asp Arg Asp
 225 230 235 240

Asp Asn Lys Val Tyr Phe Phe Phe Thr Glu Lys Ala Leu Glu Ala Glu
 245 250 255

7

Asn Asn Ala His Ala Ile Tyr Thr Arg Val Gly Arg Leu Cys Val Asn
 260 265 270

Asp Val Gly Gly Gln Arg Ile Leu Val Asn Lys Trp Ser Thr Phe Leu
 275 280 285

Lys Ala Arg Leu Val Cys Ser Val Pro Gly Met Asn Gly Ile Asp Thr
 290 295 300

Tyr Phe Asp Glu Leu Glu Asp Val Phe Leu Leu Pro Thr Arg Asp His
 305 310 315 320

Lys Asn Pro Val Ile Phe Gly Leu Phe Asn Thr Thr Ser Asn Ile Phe
 325 330 335

Arg Gly His Ala Ile Cys Val Tyr His Met Ser Ser Ile Arg Ala Ala
 340 345 350

Phe Asn Gly Pro Tyr Ala His Lys Glu Gly Pro Glu Tyr His Trp Ser
 355 360 365

Val Tyr Glu Gly Lys Val Pro Tyr Pro Arg Pro Gly Ser Cys Ala Ser
 370 375 380

Lys Val Asn Gly Gly Arg Tyr Gly Thr Thr Lys Asp Tyr Pro Asp Asp
 385 390 395 400

Ala Ile Arg Phe Ala Arg Ser His Pro Leu Met Tyr Gln Ala Ile Lys
 405 410 415

Pro Ala His Lys Lys Pro Ile Leu Val Lys Thr Asp Gly Lys Tyr Asn
 420 425 430

Leu Lys Gln Ile Ala Val Asp Arg Val Glu Ala Glu Asp Gly Gln Tyr
 435 440 445

Asp Val Leu Phe Ile Gly Thr Asp Asn Gly Ile Val Leu Lys Val Ile
 450 455 460

Thr Ile Tyr Asn Gln Glu Met Glu Ser Met Glu Glu Val Ile Leu Glu

8

465 470 475 480

Glu Leu Gln Ile Phe Lys Asp Pro Val Pro Ile Ile Ser Met Glu Ile
 485 490 495

Ser Ser Lys Arg Gln Gln Leu Tyr Ile Gly Ser Ala Ser Ala Val Ala
 500 505 510

Gln Val Arg Phe His His Cys Asp Met Tyr Gly Ser Ala Cys Ala Asp
 515 520 525

Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ile Ser Cys
 530 535 540

Ser Arg Tyr Tyr Pro Thr Gly Thr His Ala Lys Arg Arg Phe Arg Arg
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Gln Asp Val Arg His Gly Asn Ala Ala Gln Gln Cys Phe Gly Gln Gln
 565 570 575

Phe Val Gly Asp Ala Leu Asp Lys Thr Glu Glu His Leu Ala Tyr Gly
 580 585 590

Ile Glu Asn Asn Ser Thr Leu Leu Glu Cys Thr Pro Arg Ser Leu Gln
 595 600 605

Ala Lys Val Ile Trp Phe Val Gln Lys Gly Arg Glu Thr Arg Lys Glu
 610 615 620

Glu Val Lys Thr Asp Asp Arg Val Val Lys Met Asp Leu Gly Leu Leu
 625 630 635 640

Phe Leu Arg Leu His Lys Ser Asp Ala Gly Thr Tyr Phe Cys Gln Thr
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Val Glu His Ser Phe Val His Thr Val Arg Lys Ile Thr Leu Glu Val
 660 665 670

Val Glu Glu Glu Lys Val Glu Asp Met Phe Asn Lys Asp Asp Glu Glu
 675 680 685

Asp Arg His His Arg Met Pro Cys Pro Ala Gln Ser Ser Ile Ser Gln
 690 695 700

Gly Ala Lys Pro Trp Tyr Lys Glu Phe Leu Gln Leu Ile Gly Tyr Ser
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Asn Phe Gln Arg Val Glu Glu Tyr Cys Glu Lys Val Trp Cys Thr Asp
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Arg Lys Arg Lys Lys Leu Lys Met Ser Pro Ser Lys Trp Lys Tyr Ala
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Asn Pro Gln Glu Lys Lys Leu Arg Ser Lys Pro Glu His Tyr Arg Leu
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Pro Arg His Thr Leu Asp Ser
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<210> 3

<211> 560

<212> PRT

<213> 61 kDa proteolytic fragment of mouse Sema3E

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Leu Arg Leu Ser His Lys Glu Leu Leu Glu Leu Asn Arg Thr Ser Ile
 35 40 45

Phe Gln Ser Pro Leu Gly Phe Leu Asp Leu His Thr Met Leu Leu Asp
 50 55 60

10

Glu Tyr Gln Glu Arg Leu Phe Val Gly Gly Arg Asp Leu Val Tyr Ser
65 70 75 80

Leu Asn Leu Glu Arg Val Ser Asp Gly Tyr Arg Glu Ile Tyr Trp Pro
85 90 95

Ser Thr Ala Val Lys Val Glu Glu Cys Ile Met Lys Gly Lys Asp Ala
100 105 110

Asn Glu Cys Ala Asn Tyr Ile Arg Val Leu His His Tyr Asn Arg Thr
115 120 125

His Leu Leu Thr Cys Ala Thr Gly Ala Phe Asp Pro His Cys Ala Phe
130 135 140

Ile Arg Val Gly His His Ser Glu Glu Pro Leu Phe His Leu Glu Ser
145 150 155 160

His Arg Ser Glu Arg Gly Arg Gly Arg Cys Pro Phe Asp Pro Asn Ser
165 170 175

Ser Phe Val Ser Thr Leu Val Gly Asn Glu Leu Phe Ala Gly Leu Tyr
180 185 190

Ser Asp Tyr Trp Gly Arg Asp Ser Ala Ile Phe Arg Ser Met Gly Lys
195 200 205

Leu Gly His Ile Arg Thr Glu His Asp Asp Glu Arg Leu Leu Lys Glu
210 215 220

Pro Lys Phe Val Gly Ser Tyr Met Ile Pro Asp Asn Glu Asp Arg Asp
225 230 235 240

Asp Asn Lys Met Tyr Phe Phe Phe Thr Glu Lys Ala Leu Glu Ala Glu
245 250 255

Asn Asn Ala His Thr Ile Tyr Thr Arg Val Gly Arg Leu Cys Val Asn
260 265 270

Asp Met Gly Gly Gln Arg Ile Leu Val Asn Lys Trp Ser Thr Phe Leu
 275 280 285

Lys Ala Arg Leu Val Cys Ser Val Pro Gly Met Asn Gly Ile Asp Thr
 290 295 300

Tyr Phe Asp Glu Leu Glu Asp Val Phe Leu Leu Pro Thr Arg Asp Pro
 305 310 315 320

Lys Asn Pro Val Ile Phe Gly Leu Phe Asn Thr Thr Ser Asn Ile Phe
 325 330 335

Arg Gly His Ala Val Cys Val Tyr His Met Ser Ser Ile Arg Glu Ala
 340 345 350

Phe Asn Gly Pro Tyr Ala His Lys Glu Gly Pro Glu Tyr His Trp Ser
 355 360 365

Leu Tyr Glu Gly Lys Val Pro Tyr Pro Arg Pro Gly Ser Cys Ala Ser
 370 375 380

Lys Val Asn Gly Gly Lys Tyr Gly Thr Thr Lys Asp Tyr Pro Asp Asp
 385 390 395 400

Ala Ile Arg Phe Ala Arg Ile Asp Pro Leu Met Tyr Gln Pro Ile Lys
 405 410 415

Pro Val His Lys Lys Pro Ile Leu Val Lys Thr Asp Gly Lys Tyr Asn
 420 425 430

Leu Arg Gln Leu Ala Val Asp Arg Val Glu Ala Glu Asp Gly Gln Tyr
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Asp Val Leu Phe Ile Gly Thr Asp Thr Gly Ile Val Leu Lys Val Ile
 450 455 460

Thr Ile Tyr Asn Gln Glu Thr Glu Trp Met Glu Glu Val Ile Leu Glu
 465 470 475 480

Glu Leu Gln Ile Phe Lys Asp Pro Ala Pro Ile Ile Ser Met Glu Ile

Leu Ser Leu Glu Arg Ile Ser Asp Gly Tyr Lys Glu Ile His Trp Pro
85 90 95

13

Ser Thr Ala Leu Lys Met Glu Glu Cys Ile Met Lys Gly Lys Asp Ala
 100 105 110

Gly Glu Cys Ala Asn Tyr Val Arg Val Leu His His Tyr Asn Arg Thr
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His Leu Leu Thr Cys Gly Thr Gly Ala Phe Asp Pro Val Cys Ala Phe
 130 135 140

Ile Arg Val Gly Tyr His Leu Glu Asp Pro Leu Phe His Leu Glu Ser
 145 150 155 160

Pro Arg Ser Glu Arg Gly Arg Gly Arg Cys Pro Phe Asp Pro Ser Ser
 165 170 175

Ser Phe Ile Ser Thr Leu Ile Gly Ser Glu Leu Phe Ala Gly Leu Tyr
 180 185 190

Ser Asp Tyr Trp Ser Arg Asp Ala Ala Ile Phe Arg Ser Met Gly Arg
 195 200 205

Leu Ala His Ile Arg Thr Glu His Asp Asp Glu Arg Leu Leu Lys Glu
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Pro Lys Phe Val Gly Ser Tyr Met Ile Pro Asp Asn Glu Asp Arg Asp
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Asp Asn Lys Val Tyr Phe Phe Phe Thr Glu Lys Ala Leu Glu Ala Glu
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Asn Asn Ala His Ala Ile Tyr Thr Arg Val Gly Arg Leu Cys Val Asn
 260 265 270

Asp Val Gly Gly Gln Arg Ile Leu Val Asn Lys Trp Ser Thr Phe Leu
 275 280 285

Lys Ala Arg Leu Val Cys Ser Val Pro Gly Met Asn Gly Ile Asp Thr
 290 295 300

14

Tyr Phe Asp Glu Leu Glu Asp Val Phe Leu Leu Pro Thr Arg Asp His
 305 310 315 320

Lys Asn Pro Val Ile Phe Gly Leu Phe Asn Thr Thr Ser Asn Ile Phe
 325 330 335

Arg Gly His Ala Ile Cys Val Tyr His Met Ser Ser Ile Arg Ala Ala
 340 345 350

Phe Asn Gly Pro Tyr Ala His Lys Glu Gly Pro Glu Tyr His Trp Ser
 355 360 365

Val Tyr Glu Gly Lys Val Pro Tyr Pro Arg Pro Gly Ser Cys Ala Ser
 370 375 380

Lys Val Asn Gly Gly Arg Tyr Gly Thr Thr Lys Asp Tyr Pro Asp Asp
 385 390 395 400

Ala Ile Arg Phe Ala Arg Ser His Pro Leu Met Tyr Gln Ala Ile Lys
 405 410 415

Pro Ala His Lys Lys Pro Ile Leu Val Lys Thr Asp Gly Lys Tyr Asn
 420 425 430

Leu Lys Gln Ile Ala Val Asp Arg Val Glu Ala Glu Asp Gly Gln Tyr
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Asp Val Leu Phe Ile Gly Thr Asp Asn Gly Ile Val Leu Lys Val Ile
 450 455 460

Thr Ile Tyr Asn Gln Glu Met Glu Ser Met Glu Glu Val Ile Leu Glu
 465 470 475 480

Glu Leu Gln Ile Phe Lys Asp Pro Val Pro Ile Ile Ser Met Glu Ile
 485 490 495

Ser Ser Lys Arg Gln Gln Leu Tyr Ile Gly Ser Ala Ser Ala Val Ala
 500 505 510

Gln Val Arg Phe His His Cys Asp Met Tyr Gly Ser Ala Cys Ala Asp
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Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ile Ser Cys
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Ser Arg Tyr Tyr Pro Thr Gly Thr His Ala Lys Arg Arg Phe Arg Arg
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<211> 50

<212> PRT

<213> mouse Sema3E : a fragment comprising a pro-protein
convertase cleavage site

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Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ile Ser Cys Ser Arg
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Tyr Tyr Pro Thr Gly Thr His Ala Lys Arg Arg Phe Arg Arg Gln Asp
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Val Arg His Gly Asn Ala Ala Gln Gln Cys Phe Gly Gln Gln Phe Val
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Gly Asp
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<210> 6

<211> 50

<212> PRT

<213> human SEMA3E: a fragment comprising a pro-protein
convertase cleavage site

<400> 6

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Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ile Ser Cys Ser Arg
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Tyr Tyr Pro Thr Gly Thr His Ala Lys Arg Arg Phe Arg Arg Gln Asp
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Val Arg His Gly Asn Ala Ala Gln Gln Cys Phe Gly Gln Gln Phe Val
35 40 45

Gly Asp
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<210> 7

<211> 4460

<212> DNA

<213> cDNA mouse Sema3E #Z93947

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420

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<211> 2328

<212> DNA

<213> cDNA mouse Sema3E #Z80941

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<211> 3982

<212> DNA

<213> cDNA mouse Sema3E #Z93948

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24

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27

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<211> 1200

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<213> cDNA human SEMA3E #NM012431

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600

28

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<210> 11

<211> 680

<212> PRT

<213> Plexin A1 Genbank#X87832.2: ECTO domain

<400> 11

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Gly	Val	Asn	Cys	Ser	Phe	Glu	Asp	Phe	Thr	Glu	Ser	Glu	Ser	Val	Leu
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30

Cys Leu Lys Ala Asp Pro Arg Phe Glu Cys Gly Trp Cys Val Ala Glu
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Arg Arg Cys Ser Leu Arg His His Cys Ala Ala Asp Thr Pro Ala Ser
 275 280 285

Trp Met His Ala Arg His Gly Ser Ser Arg Cys Thr Asp Pro Lys Ile
 290 295 300

Leu Lys Leu Ser Pro Glu Thr Gly Pro Arg Gln Gly Gly Thr Arg Leu
 305 310 315 320

Thr Ile Thr Gly Glu Asn Leu Gly Leu Arg Phe Glu Asp Val Arg Leu
 325 330 335

Gly Val Arg Val Gly Lys Val Leu Cys Ser Pro Val Glu Ser Glu Tyr
 340 345 350

Ile Ser Ala Glu Gln Ile Val Cys Glu Ile Gly Asp Ala Ser Ser Val
 355 360 365

Arg Ala His Asp Ala Leu Val Glu Val Cys Val Arg Asp Cys Ser Pro
 370 375 380

His Tyr Arg Ala Leu Ser Pro Lys Arg Phe Thr Phe Val Thr Pro Thr
 385 390 395 400

Phe Tyr Arg Val Ser Pro Ser Arg Gly Pro Leu Ser Gly Gly Thr Trp
 405 410 415

Ile Gly Ile Glu Gly Ser His Leu Asn Ala Gly Ser Asp Val Ala Val
 420 425 430

Ser Val Gly Gly Arg Pro Cys Ser Phe Ser Trp Arg Asn Ser Arg Glu
 435 440 445

Ile Arg Cys Leu Thr Pro Pro Gly Gln Ser Pro Gly Ser Ala Pro Ile
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31

Ile Ile Asn Ile Asn Arg Ala Gln Leu Thr Asn Pro Glu Val Lys Tyr
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Asn Tyr Thr Glu Asp Pro Thr Ile Leu Arg Ile Asp Pro Glu Trp Ser
 485 490 495

Ile Asn Ser Gly Gly Thr Leu Leu Thr Val Thr Gly Thr Asn Leu Ala
 500 505 510

Thr Val Arg Glu Pro Arg Ile Arg Ala Lys Tyr Gly Gly Ile Glu Arg
 515 520 525

Glu Asn Gly Cys Leu Val Tyr Asn Asp Thr Thr Met Val Cys Arg Ala
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Pro Ser Val Ala Asn Pro Val Arg Ser Pro Pro Glu Leu Gly Glu Arg
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Pro Asp Glu Leu Gly Phe Val Met Asp Asn Val Arg Ser Leu Leu Val
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Leu Asn Ser Thr Ser Phe Leu Tyr Tyr Pro Asp Pro Val Leu Glu Pro
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Leu Ser Pro Thr Gly Leu Leu Glu Leu Lys Pro Ser Ser Pro Leu Ile
 595 600 605

Leu Lys Gly Arg Asn Leu Leu Pro Pro Ala Pro Gly Asn Ser Arg Leu
 610 615 620

Asn Tyr Thr Val Leu Ile Gly Ser Thr Pro Cys Thr Leu Thr Val Ser
 625 630 635 640

Glu Thr Gln Leu Leu Cys Glu Ala Pro Asn Leu Thr Gly Gln His Lys
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<211> 677

<212> PRT

<213> Plexin A2 Genbank#BAA32308: ECTO domain

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35 40 45

Ser Gly Ser Gln Val Ile Cys Ile Ser Pro Gly Pro Lys Asp Val Pro
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Val Ile Pro Leu Asp Gln Asp Trp Phe Gly Leu Glu Leu Gln Leu Arg
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Ser Lys Glu Thr Gly Lys Ile Phe Val Ser Thr Glu Phe Lys Phe Tyr
85 90 95

Asn Cys Ser Ala His Gln Leu Cys Leu Ser Cys Val Asn Ser Ala Phe
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Arg Cys His Trp Cys Lys Tyr Arg Asn Leu Cys Thr His Asp Pro Thr
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Thr Cys Ser Phe Gln Glu Gly Arg Ile Asn Ile Ser Glu Asp Cys Pro
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Gln Leu Val Pro Thr Glu Glu Ile Leu Ile Pro Val Gly Glu Val Lys

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Thr Lys Ser His Gln Gln Tyr Thr Phe Val Asn Pro Ser Val Leu Ser
 385 390 395 400

Leu Asn Pro Ile Arg Gly Pro Glu Ser Gly Gly Thr Met Val Thr Ile
 405 410 415

Thr Gly His Tyr Leu Gly Ala Gly Ser Ser Val Ala Val Tyr Leu Gly
 420 425 430

Asn Gln Thr Cys Glu Phe Tyr Gly Arg Ser Met Ser Glu Ile Val Cys
 435 440 445

Val Ser Pro Pro Ser Ser Asn Gly Leu Gly Pro Val Pro Val Ser Val
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Ser Val Asp Arg Ala His Val Asp Ser Asn Leu Gln Phe Glu Tyr Ile
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Asp Asp Pro Arg Val Gln Arg Ile Glu Pro Glu Trp Ser Ile Ala Ser
 485 490 495

Gly His Thr Pro Leu Thr Ile Thr Gly Phe Asn Leu Asp Val Ile Gln
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Glu Pro Arg Ile Arg Val Lys Phe Asn Gly Lys Glu Ser Val Asn Val
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Cys Lys Val Val Asn Thr Thr Thr Leu Thr Cys Leu Ala Pro Ser Leu
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Thr Thr Asp Tyr Arg Pro Gly Leu Asp Thr Val Glu Arg Pro Asp Glu
 545 550 555 560

Phe Gly Phe Val Phe Asn Asn Val Gln Ser Leu Leu Ile Tyr Asn Asp
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35

Thr Lys Phe Ile Tyr Tyr Pro Asn Pro Thr Phe Glu Leu Leu Ser Pro
 580 585 590

Thr Gly Val Leu Asp Gln Lys Pro Gly Ser Pro Ile Ile Leu Lys Gly
 595 600 605

Lys Asn Leu Cys Pro Pro Ala Ser Gly Gly Ala Lys Leu Asn Tyr Thr
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Val Leu Ile Gly Glu Thr Pro Cys Ala Val Thr Val Ser Glu Thr Gln
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Leu Leu Cys Glu Pro Pro Asn Leu Thr Gly Gln His Lys Val Met Val
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<211> 687

<212> PRT

<213> Plexin A3 Genbank#P51805: ECTO domain

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 35 40 45

Ala Ala Glu Asn Glu Ala Val Leu Leu Pro Ser Gly Glu Leu Leu Cys
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Pro Ser Pro Ser Leu Gln Glu Leu Arg Ala Leu Thr Arg Gly His Gly
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Ala Thr Arg Thr Val Arg Leu Gln Leu Leu Ser Lys Glu Thr Gly Val
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Arg Phe Ala Gly Ala Asp Phe Val Phe Tyr Asn Cys Ser Val Leu Gln
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Ser Cys Met Ser Cys Val Gly Ser Pro Tyr Pro Cys His Trp Cys Lys
 115 120 125

Tyr Arg His Thr Cys Thr Ser Arg Pro His Glu Cys Ser Phe Gln Glu
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Gly Arg Val His Ser Pro Glu Gly Cys Pro Glu Ile Leu Pro Ser Gly
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Asp Leu Leu Ile Pro Val Gly Val Met Gln Pro Leu Thr Leu Arg Ala
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Lys Asn Leu Pro Gln Pro Gln Ser Gly Gln Lys Asn Tyr Glu Cys Val
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Val Arg Val Gln Gly Arg Gln Gln Arg Val Pro Ala Val Arg Phe Asn
 195 200 205

Ser Ser Ser Val Gln Cys Gln Asn Ala Ser Tyr Ser Tyr Glu Gly Asp
 210 215 220

Glu His Gly Asp Thr Glu Leu Asp Phe Ser Val Val Trp Asp Gly Asp
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Trp Ala Gln Arg Pro Ser Cys Gly Leu Cys Leu Lys Ala Asp Pro Arg

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Arg Leu Glu Pro Thr Trp Ser Ile Ile Asn Gly Ser Thr Ala Ile Thr
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Val Ser Gly Thr His Leu Leu Thr Val Gln Glu Pro Arg Val Arg Ala
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Lys Tyr Arg Gly Ile Glu Thr Thr Asn Thr Cys Gln Val Ile Asn Asp
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Pro Arg Ala Gln Gly Glu His Pro Asp Glu Phe Gly Phe Leu Leu Asp
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His Val Gln Thr Ala Arg Ser Leu Asn Arg Ser Ser Phe Thr Tyr Tyr
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Pro Asp Pro Ser Phe Glu Pro Leu Gly Pro Ser Gly Val Leu Asp Val
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Lys Pro Gly Ser His Val Val Leu Lys Gly Lys Asn Leu Ile Pro Ala
 610 615 620

Ala Ala Gly Ser Ser Arg Leu Asn Tyr Thr Val Leu Ile Gly Gly Gln
 625 630 635 640

Pro Cys Ser Leu Thr Val Ser Asp Thr Gln Leu Leu Cys Asp Ser Pro
 645 650 655

Ser Gln Thr Gly Arg Gln Pro Val Met Val Leu Val Gly Gly Leu Glu
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Phe Trp Leu Gly Thr Leu His Ile Ser Ala Glu Arg Ala Leu Thr
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<213> human SEMA 3E: sense primer

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22

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<213> human SEMA 3E antisense primer

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23

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<213> mouse sema 3A antisense primer

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<213> mouse sema 3A sense primer

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<213> mouse sema 3B antisense primer

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<213> mouse sema 3C antisense primer

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<213> mouse sema 3E sense primer

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<213> mouse sema 3E antisense primer: stop codon

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<213> mouse sema 3E antisense primer: read through

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<213> mouse sema 3E sense primer: mutated proteolytic site

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<211> 33

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<213> mouse sema 3E antisense primer: mutated proteolytic site

<400> 26
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<213> mouse sema 3E sense primer:PstI linker

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31

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<213> mouse sema 3E antisense primer: ApaI linker

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31

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<213> mouse sema 3E sense primer: PstI site

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29

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<213> mouse sema 3E antisense primer:NotI site

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21